

REMARKS

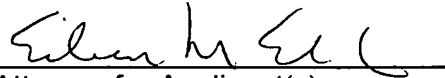
Applicants have amended the above paragraphs under 37 C.F.R. §1.822(d) to include the required SEQ ID NO identifiers. Any bolded text found in sequence data was initially present in the application as filed.

Further, applicants have submitted a new Sequence Listing in accordance with 37 C.F.R. §§1.821-1.825. The examiner is directed to two changes in SEQ ID NOS 1-2, which were shown in the original Sequence Listing filed with the instant application. Specifically, residue 407 of SEQ ID NO: 2 (previously "Ile") has been amended to comport with the disclosure of the correct residue (Ser) from the polypeptide shown in Table 4. Further support for this change can also be found in the crystal coordinate data on page 101 of the specification (SER A 437). Accordingly, the nucleotide sequence of SEQ ID NO: 1 in the originally filed Sequence Listing has been amended to correct a typographical error at position 1220, which corresponds to the second nucleotide base of the codon coding for amino acid 407 of SEQ ID NO: 2. Specifically, the "t" at position 1220 has been changed to "g", thus altering the codon from "att" to "agt". Review of the standard genetic code indicates that the *only* acceptable second nucleotide of the "ant" codon for Serine is "g". That is, the codons "aat", "act" and "att" all do not code for Serine. Since "g" is the only possible nucleotide at this position that does code for Serine, it is implicitly understood that such a change does not enter new matter.

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A Petition for Extension of Time – 1 month – is enclosed. If any required fees are missing or deficient, please charge our deposit account no. 08-2525.

Respectfully submitted,



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